

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 10/531164
Source: PC
Date Processed by STIC: 5-3-05

ENTERED



PCT

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/531,164

DATE: 05/03/2005
TIME: 11:39:36

Input Set : D:\819_seq_listing.txt
Output Set: N:\CRF4\05032005\J531164.raw

6 <110> APPLICANT: Tang, Y. Tom
7 Wang, Jian-Rui
8 Wang, Zhiwei
9 Zhou, Ping
10 Zhang, Jie
11 Ghosh, Malabika
12 Ren, Feiyan
13 Asundi, Vinod
14 Zhao, Qing A.
15 Xue, Aidong J.
16 Chen, Rui-hong
17 Wehrman, Tom
18 Ma, Yunqing
19 Wang, Dunrui
20 Weng, Gezhi
23 <120> TITLE OF INVENTION: Novel Nucleic Acids and
24 Polypeptides
28 <130> FILE REFERENCE: 819CIP/PCT
C--> 30 <140> CURRENT APPLICATION NUMBER: US/10/531,164
C--> 31 <141> CURRENT FILING DATE: 2005-04-12
33 <150> PRIOR APPLICATION NUMBER: 60/416,186
34 <151> PRIOR FILING DATE: 2002-10-02
36 <150> PRIOR APPLICATION NUMBER: PCT/US00/35017
37 <151> PRIOR FILING DATE: 2000-12-22
39 <150> PRIOR APPLICATION NUMBER: PCT/US01/02623
40 <151> PRIOR FILING DATE: 2001-01-25
42 <150> PRIOR APPLICATION NUMBER: PCT/US01/03800
43 <151> PRIOR FILING DATE: 2001-02-05
45 <150> PRIOR APPLICATION NUMBER: PCT/US01/04927
46 <151> PRIOR FILING DATE: 2001-02-26
48 <150> PRIOR APPLICATION NUMBER: PCT/US01/04941
49 <151> PRIOR FILING DATE: 2001-03-05
51 <150> PRIOR APPLICATION NUMBER: PCT/US01/08631
52 <151> PRIOR FILING DATE: 2001-03-30
54 <150> PRIOR APPLICATION NUMBER: PCT/US01/08656
55 <151> PRIOR FILING DATE: 2001-04-18
57 <150> PRIOR APPLICATION NUMBER: 10/084,643
58 <151> PRIOR FILING DATE: 2002-02-26
62 <160> NUMBER OF SEQ ID NOS: 2564
64 <170> SOFTWARE: pt_FL_genes Version 6.0
70 <210> SEQ ID NO: 1
71 <211> LENGTH: 1239
72 <212> TYPE: DNA

(pg. 6-7)

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73 <213> ORGANISM: Homo sapiens
75 <220> FEATURE:
76 <221> NAME/KEY: CDS
77 <222> LOCATION: (58)..(579)
79 <400> SEQUENCE: 1
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81  atg gct gca ggc tcc cgg acg tcc ctg ctc ctg gct ttt gcc ctg ctc      105
82  Met Ala Ala Gly Ser Arg Thr Ser Leu Leu Ala Phe Ala Leu Leu
83    1          5          10          15
85  tgc ctg ccc tgg ctt caa gag gct ggt gcc gtc caa acc gtt ccc tta      153
86  Cys Leu Pro Trp Leu Gln Glu Ala Gly Ala Val Gln Thr Val Pro Leu
87    20          25          30
89  tcc agg ctt ttt aaa gag gct atg ctc caa gcc cat cgc gca cac cag      201
90  Ser Arg Leu Phe Lys Glu Ala Met Leu Gln Ala His Arg Ala His Gln
91    35          40          45
93  ctg gcc att gac acc tac cag gag ttt ata agc tct tgg gga atg ggt      249
94  Leu Ala Ile Asp Thr Tyr Gln Glu Phe Ile Ser Ser Trp Gly Met Gly
95    50          55          60
97  gcg ggt cag ggg tgg caa gaa ggg gtg act ttc ccc cac tgg gga agt      297
98  Ala Gly Gln Gly Trp Gln Glu Gly Val Thr Phe Pro His Trp Gly Ser
99    65          70          75          80
101  aat ggg agg aga cta agg agc tca ggg ttg ttt tct gaa gcg aaa atg      345
102  Asn Gly Arg Arg Leu Arg Ser Ser Gly Leu Phe Ser Glu Ala Lys Met
103    85          90          95
105  cag gca gat gag cat agg ctg agc cag gtt ccc aga aga gta aca gtg      393
106  Gln Ala Asp Glu His Arg Leu Ser Gln Val Pro Arg Arg Val Thr Val
107    100         105         110
109  gga gct ggt ctc cag cat aga aag cag tgg tcc ttc ttg gtg ggg ggt      441
110  Gly Ala Gly Leu Gln His Arg Lys Gln Trp Ser Phe Leu Val Gly Gly
111    115         120         125
113  cct tcc cct agg aag aag cct ata tca caa agg aac aga agt att cat      489
114  Pro Ser Pro Arg Lys Lys Pro Ile Ser Gln Arg Asn Arg Ser Ile His
115    130         135         140
117  tcc tgc atg act ccc aga cct cct tct gct tct cag act cta ttc cga      537
118  Ser Cys Met Thr Pro Arg Pro Pro Ser Ala Ser Gln Thr Leu Phe Arg
119    145         150         155         160
121  cat cct cca aca tgg agg aaa cgc agc aga aat cca act tag agtgct      586
122  His Pro Pro Thr Trp Arg Lys Arg Ser Arg Asn Pro Thr
123    165         170
125  ccacatctcc ctgctgctca tcgagtcgcg gctggagccc gtgcgggtcc tcaggagtac      646
127  cttcaccaac aacctggtgt atgacacctc ggacagcgat gactatcacc tcctaaagga      706
129  cctagaggaa ggcattcaaa tgctgatggg ggtgaggggtg gcaccagggg tccccaatcc      766
131  tggaagccca ctggcttcga gggctggggg agagaaacac tgctgccctc ttttcagcag      826
133  tcaggcgctg acccaagaga actcacctta ttcttcattt cccctcgtga atcctccagg      886
135  cctttctcta caccctgaag gggaaggagg aaaatggata aatgagagag ggaggggaaca      946
137  gtgcccaagc gcttggtctc tccttctctt gcttcacttt gcagaggctg gaagacggca      1006
139  gccacctgac tgggcagacc ctcaagcaga cctacagcaa gtttgacaca aactcgaca      1066
141  accatgacgc actgctcaag aactacgggc tgctccactg cttcaggaag gacatggaca      1126
143  aggtcgagac attcctgcgc atggtgcagt gccgctctgt ggagggcagc tgtggcttct      1186

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145 aggggccccgc gtggcatcct gtgacccccccc cccagccccccc ccctcgcct gca 1239
150 <210> SEQ ID NO: 2
151 <211> LENGTH: 1015
152 <212> TYPE: DNA
153 <213> ORGANISM: Homo sapiens
155 <220> FEATURE:
156 <221> NAME/KEY: CDS
157 <222> LOCATION: (58)..(828)
159 <400> SEQUENCE: 2
160 cggcagcagc gactccccgc accactcagg gtccctgtgga cagctcacct agcggca 57
161 atg gct gca ggc tcc cgg acg tcc ctg ctc ctg gct ttt gcc ctg ctc 105
162 Met Ala Ala Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Ala Leu Leu
163 1 5 10 15
165 tgc ctg ccc tgg ctt caa gag gct ggt gcc gtc caa acc gtt ccc tta 153
166 Cys Leu Pro Trp Leu Gln Glu Ala Gly Ala Val Gln Thr Val Pro Leu
167 20 25 30
169 tcc agg ctt ttt aaa gag gct atg ctc caa gcc cat cgc gca cac cag 201
170 Ser Arg Leu Phe Lys Glu Ala Met Leu Gln Ala His Arg Ala His Gln
171 35 40 45
173 ctg gcc att gac acc tac cag gag ttt gaa gaa gcc tat atc aca aag 249
174 Leu Ala Ile Asp Thr Tyr Gln Glu Phe Glu Glu Ala Tyr Ile Thr Lys
175 50 55 60
177 gaa cag aag tat tca ttc ctg cat gac tcc cag acc tcc ttc tgc ttc 297
178 Glu Gln Lys Tyr Ser Phe Leu His Asp Ser Gln Thr Ser Phe Cys Phe
179 65 70 75 80
181 tca gac tct att ccg aca tcc tcc aac atg gag gaa acg cag cag aaa 345
182 Ser Asp Ser Ile Pro Thr Ser Ser Asn Met Glu Glu Thr Gln Gln Lys
183 85 90 95
185 tcc aac tta gag ctg ctc cac atc tcc ctg ctg ctc atc gag tcg cgg 393
186 Ser Asn Leu Glu Leu Leu His Ile Ser Leu Leu Leu Ile Glu Ser Arg
187 100 105 110
189 ctg gag ccc gtg cgg ttc ctc agg agt acc ttc acc aac aac ctg gtg 441
190 Leu Glu Pro Val Arg Phe Leu Arg Ser Thr Phe Thr Asn Asn Leu Val
191 115 120 125
193 tat gac acc tcg gac agc gat gac tat cac ctc cta aag gac cta gag 489
194 Tyr Asp Thr Ser Asp Ser Asp Asp Tyr His Leu Leu Lys Asp Leu Glu
195 130 135 140
197 gaa ggc atc caa atg ctg atg ggg gtg agg gtg gca cca ggg gtc ccc 537
198 Glu Gly Ile Gln Met Leu Met Gly Val Arg Val Ala Pro Gly Val Pro
199 145 150 155 160
201 aat cct gga agc cca ctg gct tcg agg gct ggg gga gag aaa cac tgc 585
202 Asn Pro Gly Ser Pro Leu Ala Ser Arg Ala Gly Gly Glu Lys His Cys
203 165 170 175
205 tgc cct ctt ttc agc agt cag gcg ctg acc caa gag aac tca cct tat 633
206 Cys Pro Leu Phe Ser Ser Gln Ala Leu Thr Gln Glu Asn Ser Pro Tyr
207 180 185 190
209 tct tca ttt ccc ctc gtg aat cct cca ggc ctt tct cta cac cct gaa 681
210 Ser Ser Phe Pro Leu Val Asn Pro Pro Gly Leu Ser Leu His Pro Glu
211 195 200 205

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213 ggg gaa gga gga aaa tgg ata aat gag aga ggg agg gaa cag tgc cca      729
214 Gly Glu Gly Gly Lys Trp Ile Asn Glu Arg Gly Arg Glu Gln Cys Pro
215      210      215      220
217 agc gct tgg tct ctc ctt ctc ttg ctt cac ttt gca gag gct gga aga      777
218 Ser Ala Trp Ser Leu Leu Leu Leu Leu His Phe Ala Glu Ala Gly Arg
219 225      230      235      240
221 cgg cag cca cct gac tgg gca gac cct caa gca gac cta cag caa gtt      825
222 Arg Gln Pro Pro Asp Trp Ala Asp Pro Gln Ala Asp Leu Gln Val
223      245      250      255
225 tga caca aactcgcaca accatgacgc actgctcaag aactacgggc tgctccactg      882
229 cttcaggaag gacatgggaca aggtcgagac attcctgcgc atggtgcagt gccgctctgt      942
231 ggagggcagc tgtggttctt aggggcccgc gtggcatcct gtgacccccccc cccagccccccc 1002
233 ccctcgccct gca      1015
238 <210> SEQ ID NO: 3
239 <211> LENGTH: 997
240 <212> TYPE: DNA
241 <213> ORGANISM: Homo sapiens
243 <220> FEATURE:
244 <221> NAME/KEY: CDS
245 <222> LOCATION: (64)..(120)
247 <400> SEQUENCE: 3
248 gagcatccca aggcccgaact ccccgcacca ctcagggtcc tgtggacagc tcacctagcg      60
250 gca atg gct gca gga aga agc cta tat cac aaa gga aca gaa gta ttc      108
251 Met Ala Ala Gly Arg Ser Leu Tyr His Lys Gly Thr Glu Val Phe
252      1      5      10      15
254 att cct gca tga ctc ccagacctcc ttctgcttct cagactctat tccgacatcc      163
255 Ile Pro Ala
258 tccaacatgg aggaaacgca gcagaaatcc aacttagagc tgctccacat ctccctgctg      223
260 ctcacatgag cgcggctgga gcccgtgcgg ttcctcagga gtaccttcac caacaacctg      283
262 gtgtatgaca cctcggacag cgatgactat cacctcctaa aggacctaga ggaaggcatc      343
264 caaatgctga tggggaggct ggaagacggc agccacctga ctgggcagac cctcaagcag      403
266 acctacagca agtttgacac aaactcgcac aaccatgacg cactgctcaa gaactacggg      463
268 ctgctccact gcttcaggaa ggacatggac aaggctcgaga cattcctgcg catggtgcag      523
270 tgccgctctg tggagggcag ctgtggcttc taggggcccg cgtggcatcc tgtgacctct      583
272 cccagtgccc tcttccctgg gccctgaagg tgccattccc aggggcccac acaaaaggcct      643
274 ggtccttaat taacacttta acggttgga tgggccagaa aaaagagaca gaacaaacaa      703
276 cgaacaacac accatttgtg gcccggcacc gacgcccaca ggaacaagcg ttgcaagaac      763
278 ccaccgcgat ggagtggacg cgcggagccg ccacagtgtg gtgaacggca gcaagggtgtg      823
280 ccaaaaggag gtgacccagg aggacaccgc ggcaggacac aagggtggg ataccagca      883
282 ctataaaaaa gccgcggggg acacacgaca gctgtgtaga acacccagc agagcgtgcc      943
284 cggaggccaa gaggacataa tcacaggagg ccacagcgac ggccgataaa tacg      997
289 <210> SEQ ID NO: 4
290 <211> LENGTH: 987
291 <212> TYPE: DNA
292 <213> ORGANISM: Homo sapiens
294 <220> FEATURE:
295 <221> NAME/KEY: CDS
296 <222> LOCATION: (1)..(771)
298 <400> SEQUENCE: 4

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299	atg gct cca ggc tcc cgg acg tcc ctg ctc ctg gct ttt gcc ctg ctc	48
300	Met Ala Pro Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Ala Leu Leu	
301	1 5 10 15	
303	tgc ctg ccc tgg ctt caa gag gct ggt gcc gtc caa acc gtt ccg tta	96
304	Cys Leu Pro Trp Leu Gln Glu Ala Gly Ala Val Gln Thr Val Pro Leu	
305	20 25 30	
307	tcc agg ctt ttt gac cac gct atg ctc caa gcc cat cgc gcg cac cag	144
308	Ser Arg Leu Phe Asp His Ala Met Leu Gln Ala His Arg Ala His Gln	
309	35 40 45	
311	ctg gcc att gac acc tac cag gag ttt gaa gaa acc tat atc cca aag	192
312	Leu Ala Ile Asp Thr Tyr Gln Glu Phe Glu Glu Thr Tyr Ile Pro Lys	
313	50 55 60	
315	gac cag aag tat tca ttc ctg cat gac tcc cag acc tcc ttc tgc ttc	240
316	Asp Gln Lys Tyr Ser Phe Leu His Asp Ser Gln Thr Ser Phe Cys Phe	
317	65 70 75 80	
319	tca gac tct att ccg aca ccc tcc aac atg gag gaa acg caa cag aaa	288
320	Ser Asp Ser Ile Pro Thr Pro Ser Asn Met Glu Glu Thr Gln Gln Lys	
321	85 90 95	
323	tcc aat cta gag ctg ctc cgc atc tcc ctg ctg ctc atc gag tcg tgg	336
324	Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu Leu Leu Ile Glu Ser Trp	
325	100 105 110	
327	ctg gag ccc gtg cgg ttc ctc agg agt atg ttc gcc aac aac ctg gtg	384
328	Leu Glu Pro Val Arg Phe Leu Arg Ser Met Phe Ala Asn Asn Leu Val	
329	115 120 125	
331	tat gac acc tcg gac agc gat gac tat cac ctc cta aag gac cta gag	432
332	Tyr Asp Thr Ser Asp Ser Asp Asp Tyr His Leu Leu Lys Asp Leu Glu	
333	130 135 140	
335	gaa ggc atc caa acg ctg atg ggg gtg agg gtg gcg cca ggg gtc acc	480
336	Glu Gly Ile Gln Thr Leu Met Gly Val Arg Val Ala Pro Gly Val Thr	
337	145 150 155 160	
339	aat cct gga acc cca ctg gct tcg agg gct ggg gga gag aaa tac tgc	528
340	Asn Pro Gly Thr Pro Leu Ala Ser Arg Ala Gly Gly Glu Lys Tyr Cys	
341	165 170 175	
343	tgc cct ctt ttt agc agt aag gcg ctg acc caa gag aac tca cct tat	576
344	Cys Pro Leu Phe Ser Ser Lys Ala Leu Thr Gln Glu Asn Ser Pro Tyr	
345	180 185 190	
347	tct tca ttt cgc ctg gtg aat cct cca ggc ctt tct cta cac cct gaa	624
348	Ser Ser Phe Arg Leu Val Asn Pro Pro Gly Leu Ser Leu His Pro Glu	
349	195 200 205	
351	ggg gag gga gga aaa tgg ata aat gag aga ggg agg gaa cag tgc cca	672
352	Gly Glu Gly Gly Lys Trp Ile Asn Glu Arg Gly Arg Glu Gln Cys Pro	
353	210 215 220	
355	agc gct tgg cct ctc ctt ctc ttc ctt cac ttt gca gag gct gga aga	720
356	Ser Ala Trp Pro Leu Leu Leu Phe Leu His Phe Ala Glu Ala Gly Arg	
357	225 230 235 240	
359	cgg cag ccg ccg gac tgg gca gat cct caa gca gac cta cag caa gtt	768
360	Arg Gln Pro Pro Asp Trp Ala Asp Pro Gln Ala Asp Leu Gln Gln Val	
361	245 250 255	
363	tga caca aactcgcaca accatgacgc actgctcaag aactacgggc tgctctactg	825

RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:18; N Pos. 8,38
Seq#:28; N Pos. 1092
Seq#:36; N Pos. 162,357
Seq#:48; N Pos. 2817
Seq#:56; N Pos. 34
Seq#:78; N Pos. 1489,1491,1493
Seq#:83; N Pos. 6,7,8
Seq#:116; N Pos. 1
Seq#:122; N Pos. 746
Seq#:128; N Pos. 2247,2448,2449,2450,2451,2452,2457
Seq#:133; N Pos. 1758
Seq#:143; N Pos. 395
Seq#:159; N Pos. 1980,2054
Seq#:176; N Pos. 2851,2866
Seq#:183; N Pos. 1952,1966
Seq#:184; N Pos. 1622,1636,1644,1658
Seq#:205; N Pos. 15,29,30,31
Seq#:211; N Pos. 1582,1652
Seq#:215; N Pos. 1923,1924,1925,1926,1927,1928,1929,1930,1931,1932,1933
Seq#:215; N Pos. 1934,1935,1936,1937,1938,1939,1940,1941,1942,1943,1944
Seq#:215; N Pos. 1945
Seq#:223; N Pos. 6,7
Seq#:239; N Pos. 818,823,836,847
Seq#:242; N Pos. 2060
Seq#:245; N Pos. 10
Seq#:256; N Pos. 12,33,34,35,36,41
Seq#:257; N Pos. 26
Seq#:258; N Pos. 26
Seq#:302; N Pos. 19,20,21
Seq#:309; N Pos. 1081
Seq#:319; N Pos. 22,29,59
Seq#:326; N Pos. 290
Seq#:331; N Pos. 19
Seq#:372; N Pos. 756
Seq#:378; N Pos. 1242
Seq#:383; N Pos. 11
Seq#:423; N Pos. 2600
Seq#:452; N Pos. 1439,1441,1443
Seq#:470; N Pos. 1823,1827,1866,1872,1876
Seq#:535; N Pos. 587
Seq#:549; N Pos. 1928
Seq#:554; N Pos. 2013
Seq#:599; N Pos. 6,37,38,205,231
Seq#:602; N Pos. 13

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Seq#:605; N Pos. 3852,3857,3858,3896
Seq#:607; N Pos. 3072,3073,3074,3075,3076,3077,3078,3079,3080,3081,3082
Seq#:607; N Pos. 3083,3084,3085,3086,3087,3088,3089,3090,3091,3092,3093
Seq#:607; N Pos. 3094,3095
Seq#:651; N Pos. 7,8,9,10,11,12,28
Seq#:1374; N Pos. 745,804,805,806,807,808,809,810,811,812,813,814,815,816
Seq#:1374; N Pos. 817,818,819,820,821,822,823,824,825,826,827,828,829,830

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 80
Seq#:2; Line(s) 160
Seq#:8; Line(s) 831
Seq#:13; Line(s) 1536
Seq#:72; Line(s) 14760
Seq#:79; Line(s) 16543
Seq#:103; Line(s) 19937
Seq#:107; Line(s) 20318
Seq#:136; Line(s) 24652
Seq#:144; Line(s) 25490
Seq#:146; Line(s) 25777
Seq#:149; Line(s) 26105
Seq#:152; Line(s) 26553
Seq#:165; Line(s) 28905
Seq#:176; Line(s) 30637
Seq#:231; Line(s) 40293
Seq#:242; Line(s) 41573
Seq#:246; Line(s) 42104
Seq#:248; Line(s) 42353
Seq#:279; Line(s) 47172
Seq#:281; Line(s) 47535
Seq#:296; Line(s) 50692
Seq#:302; Line(s) 51385
Seq#:305; Line(s) 51631
Seq#:344; Line(s) 59516
Seq#:345; Line(s) 59698
Seq#:391; Line(s) 67770
Seq#:398; Line(s) 69470
Seq#:403; Line(s) 70930
Seq#:404; Line(s) 71016
Seq#:405; Line(s) 71080
Seq#:406; Line(s) 71140
Seq#:407; Line(s) 71176
Seq#:494; Line(s) 82974
Seq#:502; Line(s) 83910
Seq#:523; Line(s) 87097
Seq#:557; Line(s) 91904

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Seq#:575; Line(s) 94124
Seq#:585; Line(s) 95177
Seq#:618; Line(s) 100872
Seq#:619; Line(s) 100915
Seq#:632; Line(s) 103684
Seq#:636; Line(s) 104084
Seq#:640; Line(s) 104587
Seq#:658; Line(s) 106533
Seq#:664; Line(s) 107555
Seq#:682; Line(s) 110706
Seq#:1974; Line(s) 181376
Seq#:1979; Line(s) 181553
Seq#:1985; Line(s) 181762
Seq#:1996; Line(s) 182183

VERIFICATION SUMMARY

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Input Set : D:\819_seq_listing.txt

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L:30 M:270 C: Current Application Number differs, Replaced Current Application Number
 L:31 M:271 C: Current Filing Date differs, Replaced Current Filing Date
 L:2353 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:0
 L:5287 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28 after pos.:1052
 L:7002 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36 after pos.:120
 M:341 Repeated in SeqNo=36
 L:10403 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:48 after pos.:2779
 L:11392 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:56 after pos.:0
 L:16518 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:78 after pos.:1443
 L:16867 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:83 after pos.:0
 L:21495 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:116 after pos.:0
 L:22142 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:122 after pos.:692
 L:22663 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:128 after pos.:2226
 M:341 Repeated in SeqNo=128
 L:24415 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:133 after pos.:1700
 L:25471 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:143 after pos.:353
 L:27666 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:159 after pos.:1957
 M:341 Repeated in SeqNo=159
 L:30792 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:176 after pos.:2804
 M:341 Repeated in SeqNo=176
 L:31875 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:183 after pos.:1950
 L:32013 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:184 after pos.:1606
 L:35212 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:205 after pos.:0
 L:36427 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:211 after pos.:1542
 M:341 Repeated in SeqNo=211
 L:37350 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:215 after pos.:1872
 M:341 Repeated in SeqNo=215
 L:38267 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:223 after pos.:0
 L:41421 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:239 after pos.:779
 M:341 Repeated in SeqNo=239
 L:41712 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:242 after pos.:2004
 L:42009 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:245 after pos.:0
 L:43089 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:256 after pos.:0
 L:43297 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:257 after pos.:0
 L:43479 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:258 after pos.:0
 L:51385 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:302 after pos.:0
 L:52515 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:309 after pos.:1053
 L:54937 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:319 after pos.:0
 L:56587 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:326 after pos.:248
 L:57108 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:331 after pos.:0
 L:65109 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:372 after pos.:724
 L:65867 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:378 after pos.:1213
 L:66590 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:383 after pos.:0
 L:73889 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:423 after pos.:2557
 L:77743 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:452 after pos.:1386
 L:79945 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:470 after pos.:1795
 M:341 Repeated in SeqNo=470
 L:88570 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:535 after pos.:553

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/531,164

DATE: 05/03/2005

TIME: 11:39:37

Input Set : D:\819_seq_listing.txt

Output Set: N:\CRF4\05032005\J531164.raw

L:90700 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:549 after pos.:1897
L:91380 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:554 after pos.:1989
L:96870 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:599 after pos.:0
M:341 Repeated in SeqNo=599